

10	30	50
GTGAAGAGCCAGAGTCCTCCAAGGTGAAGCTGGACTGAATATTTCTGTCCATAAGACTAT		
70	90	110
TAGAATCCCCCAAAGTGGGATACCAGTGAGGACCTCACCAGCAGCTGCTGTCTCTCCAAT		
130	150	170
GCAGCTCCACAGGGCCTGTGAGCAGGGCTGGCTATGAGATCCTGCCCTGAAGAGCAGTAC		
	M R S C P E E Q Y	
190	210	230
TGGGCTGCTCTGCTAGGCACCTGCATGTTCTGCAAAGCCATCTGCAACCATCAGAGCCAG		
W A A L L G T C M F C K A I C N H Q S Q		
250	270	290
CGCACCTGTGCAGCCTCCTGCGGTGAGTTCTGGGACCTGAGCCCAGGGGACAGTGTGATC		
R T C A A S C G E F W D L S P G D S V I		
310	330	350
ACCCCCAACGCCTGTCCCCAGAGCACCTCTGGCCCCACAGTCAGGTGGCTGAGGAGAGG		
T P N A C P Q S T L W P H S Q V A E E R		
370	390	410
ATGGCAGGAGGAGATGTACAGTGTGGCACCTCTTATCCCTCCACCTTCCTGCTCTGGCCA		
M A G G D V Q C G T S Y P S T F L L W P		
430	450	470
CACTGCCTCCTTTTCAGTGTGGAACATGCCATGTTCTTCCCTGCCTCGGGTTCTTTGCACA		
H C L L S V S N M P C S S L P R V L C T		
490	510	530
TGTTGTTCCCGCTGCCTGGAATGCATGCTCTCTATCATCTTCCCTCAGCTCCCTCCTACC		
C C S R C L E C M L S I I F P Q L P P T		

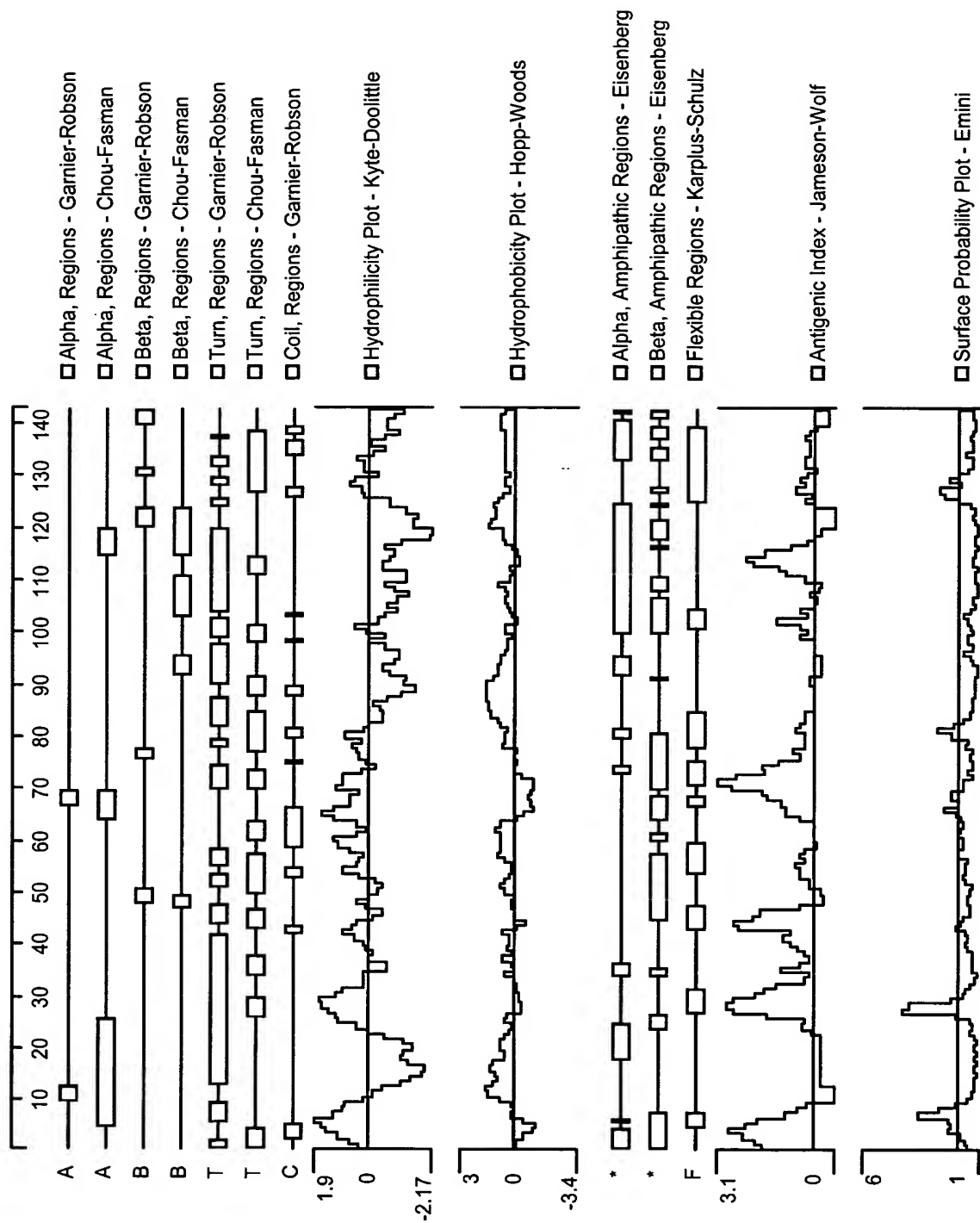
**Figure 1A**

550	570	590
CAACTTTCAGGTCTCGGCCCAAACATCGGGGGTCTCCTCTGACCACACAGTAGTACTGGG		
Q L S G L G P N I G G L L *		
610	630	650
CCCTCCTTTGTA CTAGTGTTACTTTCTTTTGAACTTTTAATTACAGAACTTACCAC		
670	690	710
ACATATACATAGAGAGGACGCACAATGATGCCCTCCTCATCCATTACCAGCTTCACAAAT		
730	750	770
CATTTAAATTCTGCCTTGTA CTTTCCCAACCAGTTGTTTTGGCTTGTGTATTTTAAAGCA		
790	810	830
AAGCMARGACCTCATATCATTTTACCTGCAGATACTGGGCCATAAAGATCTGTAAACAT		
850	870	890
AMCCCAAATATCCTATCACTGSCAGCAATAATTTATTAACATCATCTAATATTCAGGCCA		
910	930	950
TATCCAATTTTCCCTGATTGTCTTGAAA CTA TCCATTGCTTGCTGTTCTTTTTCATAAT		
970	990	1010
CTGTCTTTTTCCTTGATAGAACTTACCACAATTTGCTGTTTTGTTCTTTTGTGTGTATGT		
1030	1050	1070
GTTTCACATCTACTCAGCCACTGGACTGGGTGCTCCCTGAGGGGAGGAACCATGTCTGAC		
1090	1110	1130
TTGAACCTAGCACAGTGCCTGACACATAGTAAGTCCTTCATGAATACTTGCTGAGGGGAA		
1150	1170	1190
CTCAGAGAGGCTGAGTGACTTACCCAAGATCACACAGCTTAAAAGTGAAGATGTCAGGGT		

**Figure 1B**

1210	1230	1250
TTGAACCCAGGACTCTGACTCCTAAATCATACCCTGAACCGTTACCCATTAATGAATTAG		
1270	1290	1310
AACATTCATTGATTCATCCCACAAACATAGATGGAGTGCTCCAGCCCCATGGAAATAGGA		
1330	1350	1370
ATCTGGTGTGGCCCTTCAAGGACAGTATCATCTAATGGGAGAAATGATTGTGTGTCAAGG		
1390	1410	1430
TAGAAAGCCATAGTTGGGGCCGGGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTCAGG		
1450	1470	1490
AGGCCAAGGCGGGCGGATCACCTGAGGTGCGAAAGTTCGAGACCATCCTGACCAACAAGGA		
1510	1530	
GAAACCCTGTCTCTACTAAAAAAAAAAAAAAAAAAAA		

**Figure 1C**



**Figure 2**

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1  M-----RSCPEEQYV p1.HPMK140
1  M S G L G R S R R G G R S R Y D Q E E R F P Q G L W T G V A M R S C P E E Q Y V p1.huTACI

11 A A L L G T C M F C K A I C N H Q S Q R T C A A S C-----G E F W D p1.HPMK140
41 D P L L G T C M S E K T I C N H Q S Q R T C A A F C R S L S C R K E Q G K F Y D p1.huTACI

42 L S P G D S V I T P N A C P Q-----S T L Y P H S Q V A E E--R p1.HPMK140
81 H L L R Q C I S C A S I E G Q H P K Q C A Y F C E N K L R S P V N L P P E L R R p1.huTACI

70 M A G G D V Q C G T S Y P S T F L L W P H C L L S V S N M P C S S L P R V-- p1.HPMK140
121 Q R S G E V E N N S D N S G R Y----Q G L E H R G S E A S P A L P G L K L S p1.huTACI

107-----L C T C C S R C L E C M L S I I----- p1.HPMK140
157 A D Q V A L V Y S T L G L C L C A V L C--E F L V A V A C F L K K R G D P C S p1.huTACI

123-----F p1.HPMK140
195 C Q P R S R P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T C S F C F p1.huTACI

124 P Q- L P P T Q L S G L G P N I----- p1.HPMK140
235 P E C R A P T Q E S A V T P G T P D P T C A G R W G C H T R T T V L Q P C P H I p1.huTACI

139--G G L-----L. p1.HPMK140
275 P D S G L G I V C V P A Q E G G P G A. p1.huTACI

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Decoration 'Decoration #1': Shade (with solid black) residues that match p1.HPMK140 exactly.

**Figure 3**